RINGKASAN

Infeksi HIV yang terus meningkat di Indonesia mendorong pengembangan resistensi obat antiretroviral (ARV) yang lebih sensitif. Deteksi resistensi HIV-1 terhadap ARV dianggap penting karena kegagalan terapi sering kali disebabkan oleh keberadaan varian virus yang tidak terdeteksi melalui metode konvensional. Teknologi *Next Generation Sequencing* (NGS) berbasis *Oxford Nanopore Technologies* (ONT) dikembangkan sebagai metode yang lebih akurat dalam mendeteksi genom virus HIV penyebab resistensi, khususnya pada spesimen plasma dengan *viral load* RNA >10.000 *copies*/ml. Penerapan ONT diharapkan dapat meningkatkan ketepatan deteksi resistensi dan mendukung strategi pengobatan HIV yang lebih terpersonalisasi.

Penelitian dilaksanakan di RSPI Sulianti Saroso selama enam bulan dengan pendekatan deskriptif dan rancangan *cross-sectional*. Sampel plasma dari sepuluh pasien HIV-1 dengan *viral load* tinggi diproses melalui tahapan ekstraksi RNA, amplifikasi RT-PCR dan Nested PCR, serta validasi konsentrasi dan kemurnian asam nukleat menggunakan NanoDrop dan Qubit. DNA hasil purifikasi dipersiapkan untuk *library preparation* dan *sequencing* menggunakan perangkat GridION. Hasil *basecalling* disimpan dalam format FASTQ dan dianalisis berdasarkan *quality score* dan *coverage* menggunakan perangkat lunak MinKNOW. Evaluasi keberhasilan *sequencing* dilakukan melalui parameter Qscore (*quality score*) dan kedalaman pembacaan (*coverage*).

Hasil penelitian menunjukkan bahwa semua sampel berhasil diamplifikasi, dengan konsentrasi DNA yang cukup tinggi dan rasio kemurnian yang mendekati standar, terutama pada produk Nested PCR. Rata-rata Q score sebesar 8,1 masih berada di bawah ambang batas minimum ≥9, namun nilai *coverage* mencapai rata-rata 1435×, bahkan pada beberapa sampel lebih dari 3000×. Meskipun kualitas *basecalling* belum optimal, tingginya *coverage* memungkinkan koreksi kesalahan dan pembentukan konsensus sekuens dilakukan cukup akurat. Deteksi mutasi resistensi HIV dapat dianalisis lebih lanjut menggunakan WHO HIV *Drug Resistance Quality Control Tool* (WHOQC) serta interpretasi mutasi resistensi dapat dilakukan menggunakan platform *Stanford HIV Drug Resistance Database (HIVdb)*. Dengan demikian, penggunaan ONT dianggap layak untuk mendeteksi genom virus HIV.

Kata Kunci : HIV, *Oxford Nanopore Technology*, Genom Virus HIV, *Viral load* HIV.

SUMMARY

The increasing incidence of HIV infection in Indonesia has driven the development of more sensitive detection methods for antiretroviral (ARV) drug resistance. Detecting HIV-1 resistance to ARV is considered essential, as treatment failure is often caused by the presence of viral variants that remain undetected by conventional methods. Next Generation Sequencing (NGS) technology based on Oxford Nanopore Technologies (ONT) has been developed as a more accurate method for detecting resistance, particularly in plasma specimens with RNA *viral load*s exceeding 10,000 copies/ml. The implementation of ONT is expected to improve the accuracy of resistance mutation detection and support more personalized HIV treatment strategies.

The study was conducted at RSPI Sulianti Saroso over a six-month period using a descriptive approach and a cross-sectional design. Plasma samples from ten HIV-1 positive patients with high *viral load*s were processed through RNA extraction, amplification using RT-PCR and Nested PCR, and validation of nucleic acid concentration and purity using NanoDrop and Qubit. Purified DNA was then prepared for library construction and sequencing using the GridION platform. *Basecalling* results were stored in FASTQ format and analyzed based on quality score and sequencing depth (coverage) using MinKNOW software. The success of sequencing was evaluated through Q score and coverage parameters.

The results showed that all samples were successfully amplified, with sufficiently high DNA concentrations and purity ratios close to standard, particularly in Nested PCR products. The average Q score was 8.1, which is below the minimum threshold of ≥9, but the average coverage reached 1,435×, with several samples exceeding 3,000×. Despite the suboptimal *basecalling* quality, the high coverage enabled effective error correction and accurate consensus sequence generation. HIV drug resistance mutations can be further analyzed using the WHO HIV Drug Resistance Quality Control Tool (WHOQC), and mutation interpretation can be carried out using the Stanford HIV Drug Resistance Database (HIVdb) platform. Thus, ONT is considered feasible for detecting genome virus HIV.

Keywords : *Drug Resistance*, HIV, *Oxford Nanopore Technology*, *Viral load* HIV.